

Fig. 1

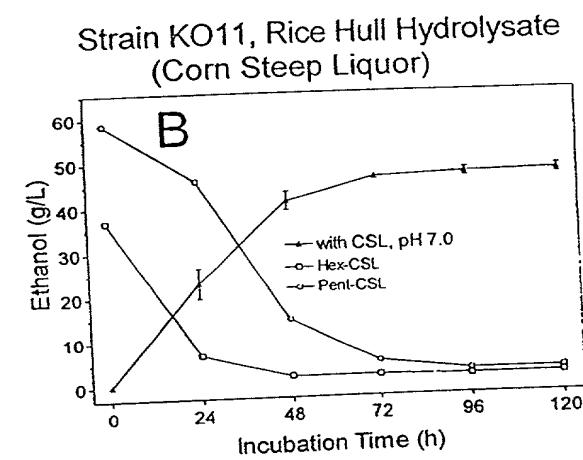
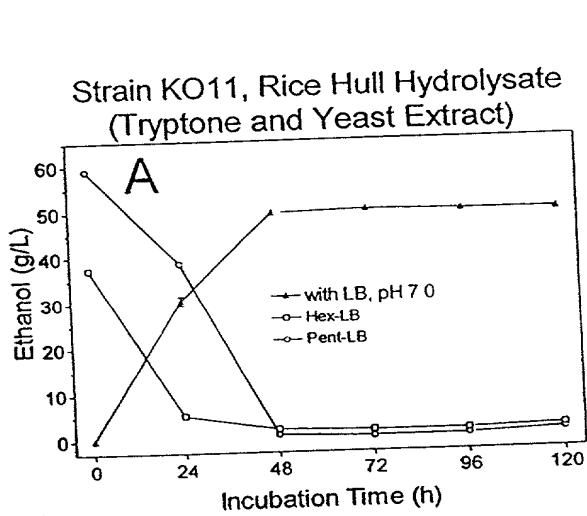


Fig. 2

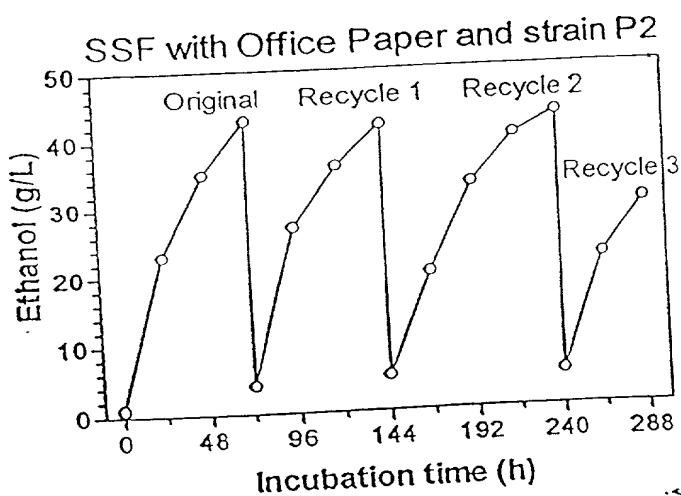


Fig. 3

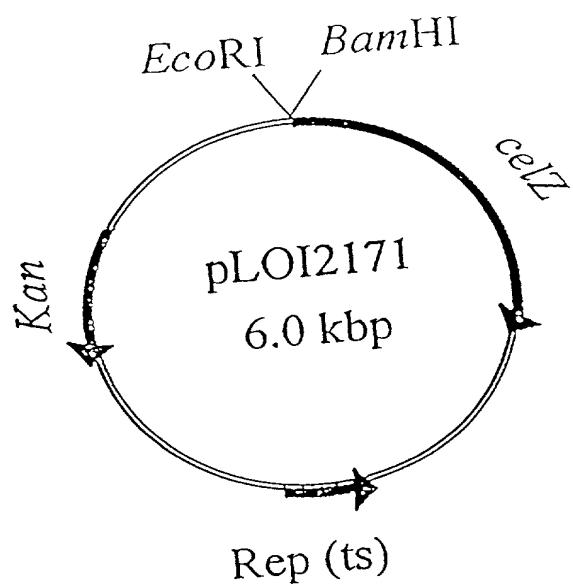


Fig. 4

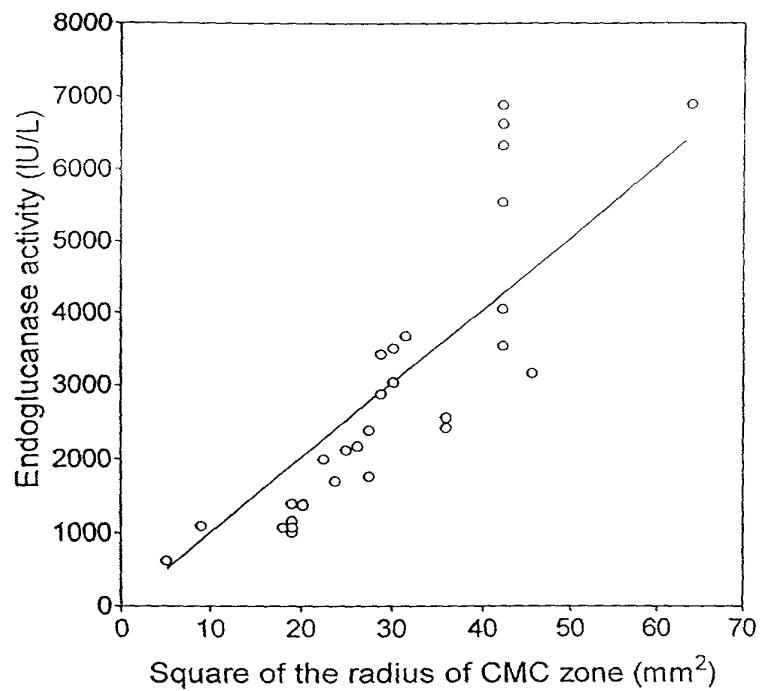


Fig. 5

-35 region #
 1051 CTTTTTCGGC ATGAGCAACC AACATTTCA AGGTATCATC CTGATGCGCA
 1101 ATATCGGCAT CGGTTAGCCA TAACCATTTC ACCTGTCCGG CGGCCTTAAT
 1151 ACCTTGATCA GATGGTTCGT GGTGTTGTTA CCTTGCCGAA GGGCACCGGT
 1201 AAAAATGTTG GCGTCGGTGT TTTGCCCGT GGCCCGAAAG CTGAAGAACGC
 1251 TAAAGCTGCT GGTGCAGAAG TTGTCGGCGC AGAAGACCTG ATGGAAGCCA
 -35 region -10 region
 1301 TTCAGGGCGG CAGCATTGAT TTCGATCGTG ATGCCCTTIA TACTGAAATT
 #
 1351 GCCTTGCCTGCCATAATGA AGCAGCCTCC GGTGTTTGG CAGATTTAAG
 Shine-Dalgarno
 1401 CGCTGCCTGA TTTTCGTgat cctcttagagt ctatgaaatg gagatgtcaatt
 celZ coding region ->
 1451 tatgcccccc tccttatccgg ataaaccatcc agtcatccgc aagcttggcc

Fig. 6

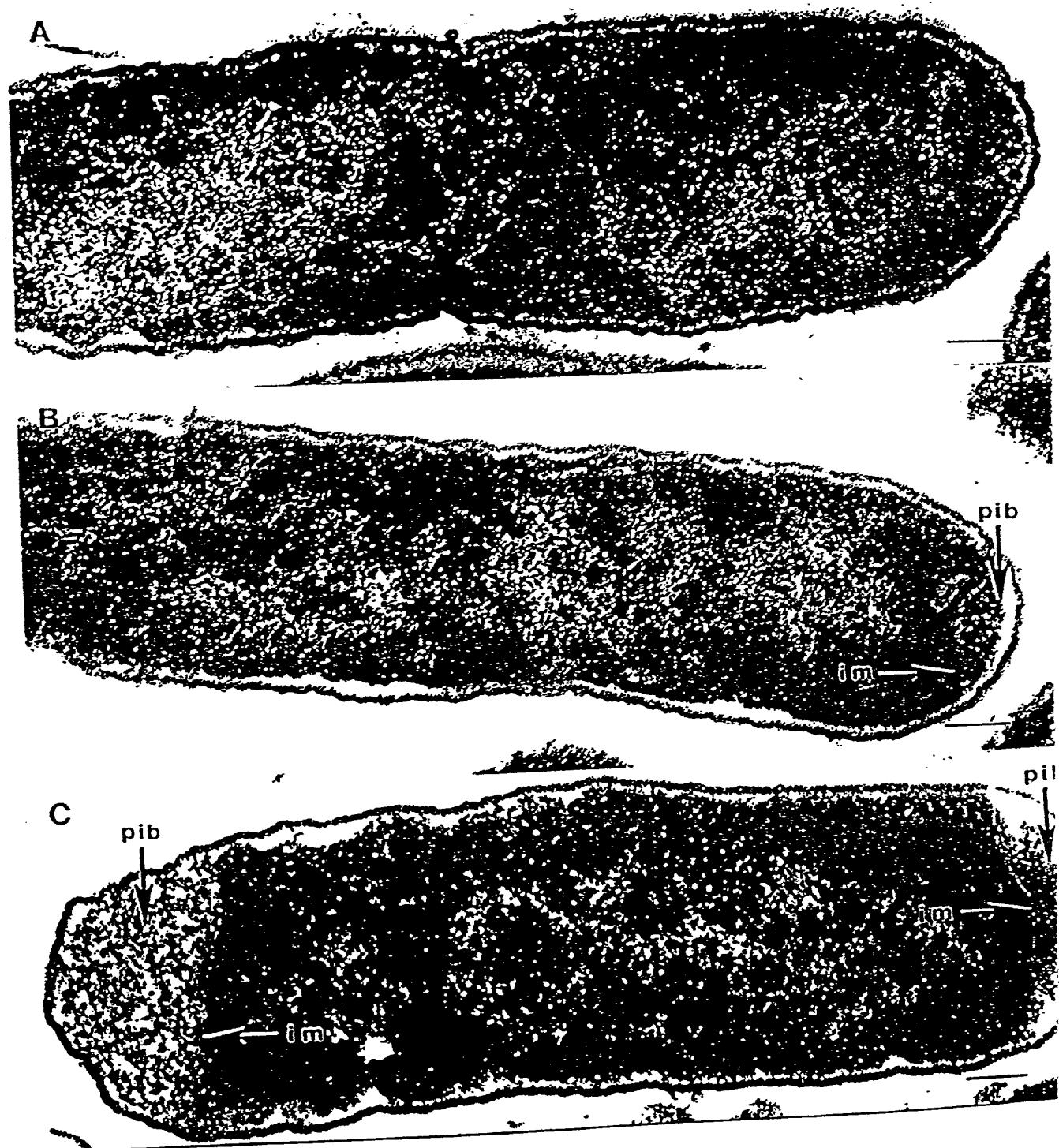


Fig. 7

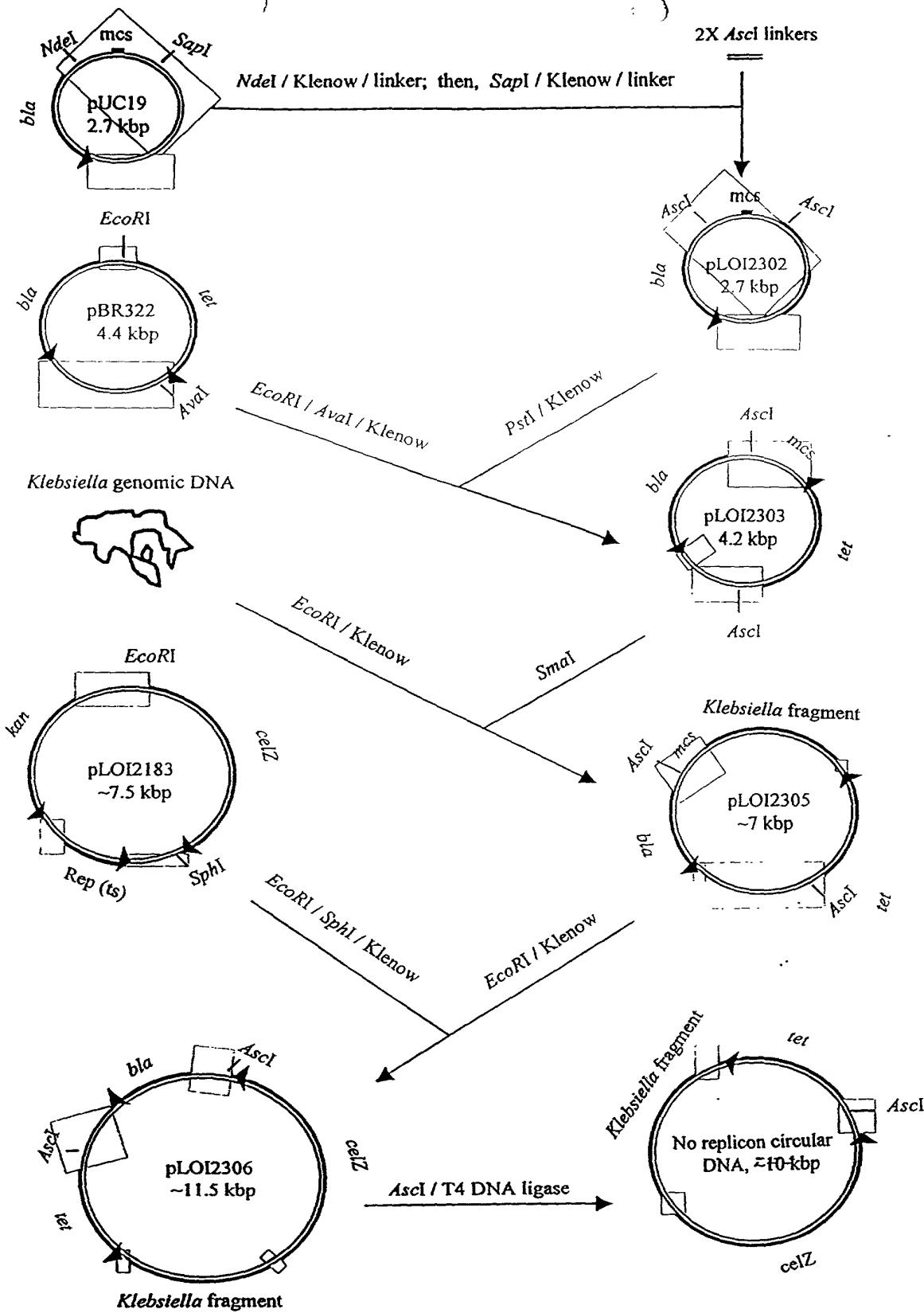


Fig. 8

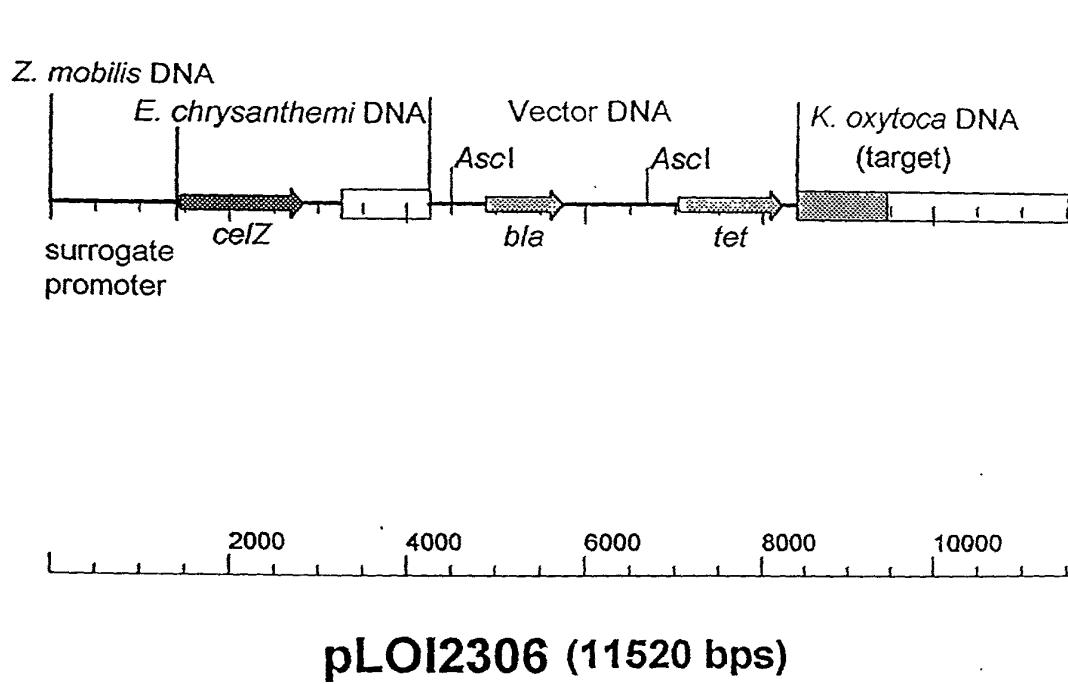


Fig. 9

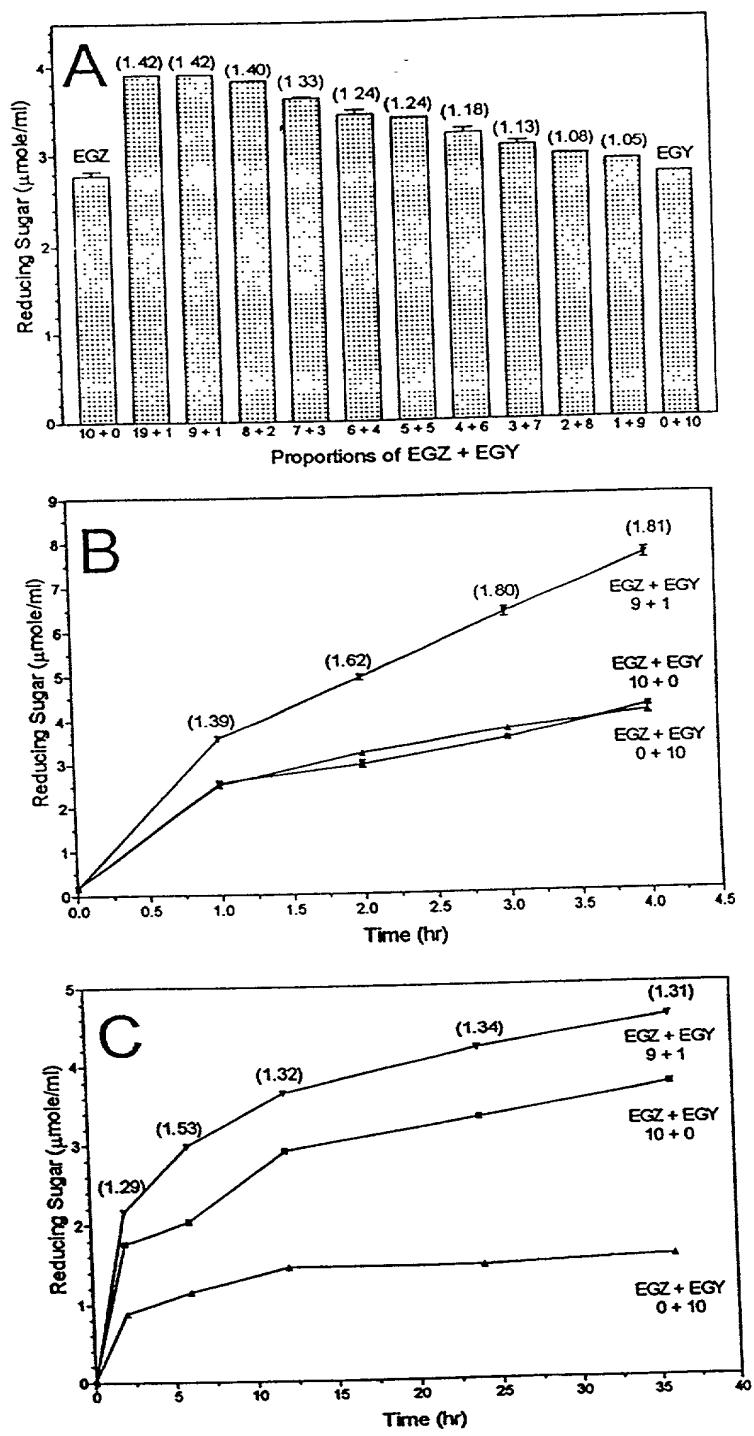


Fig. 10

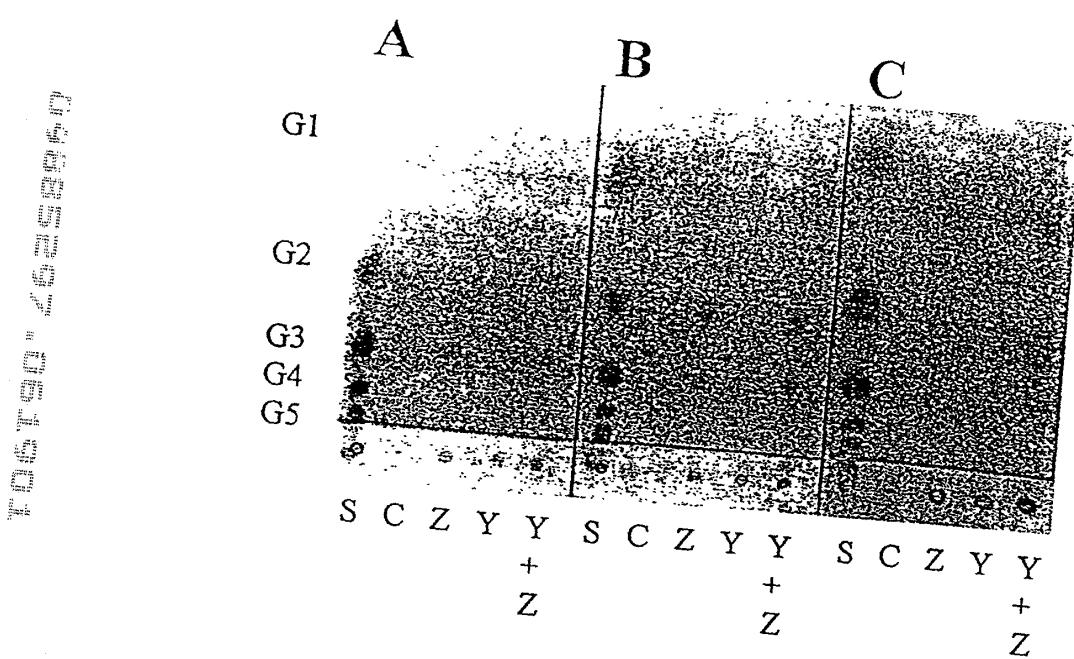


Fig. 11

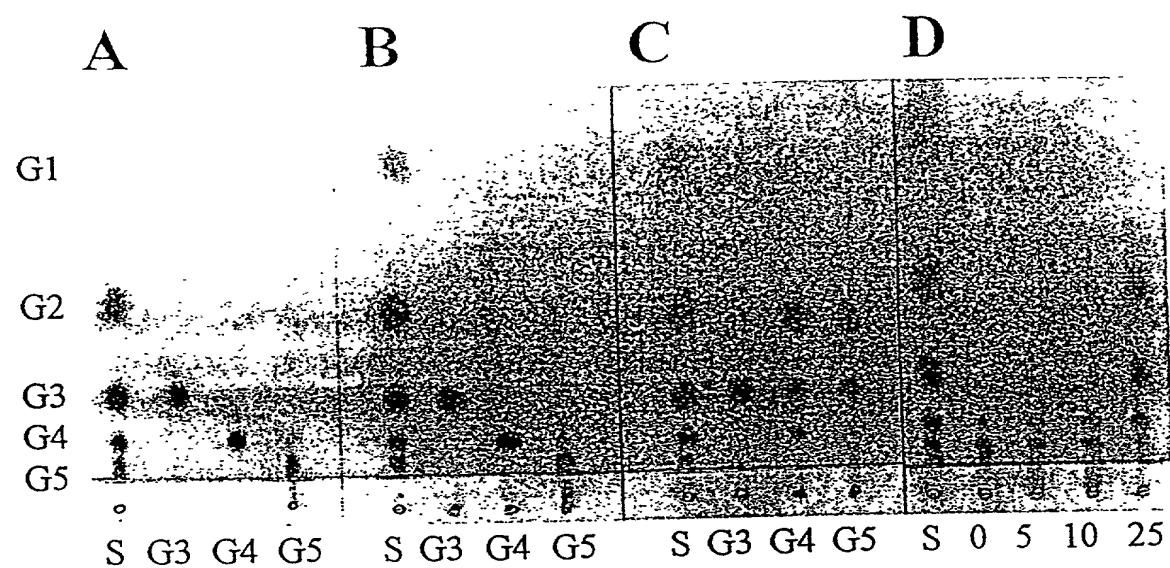


Fig. 12

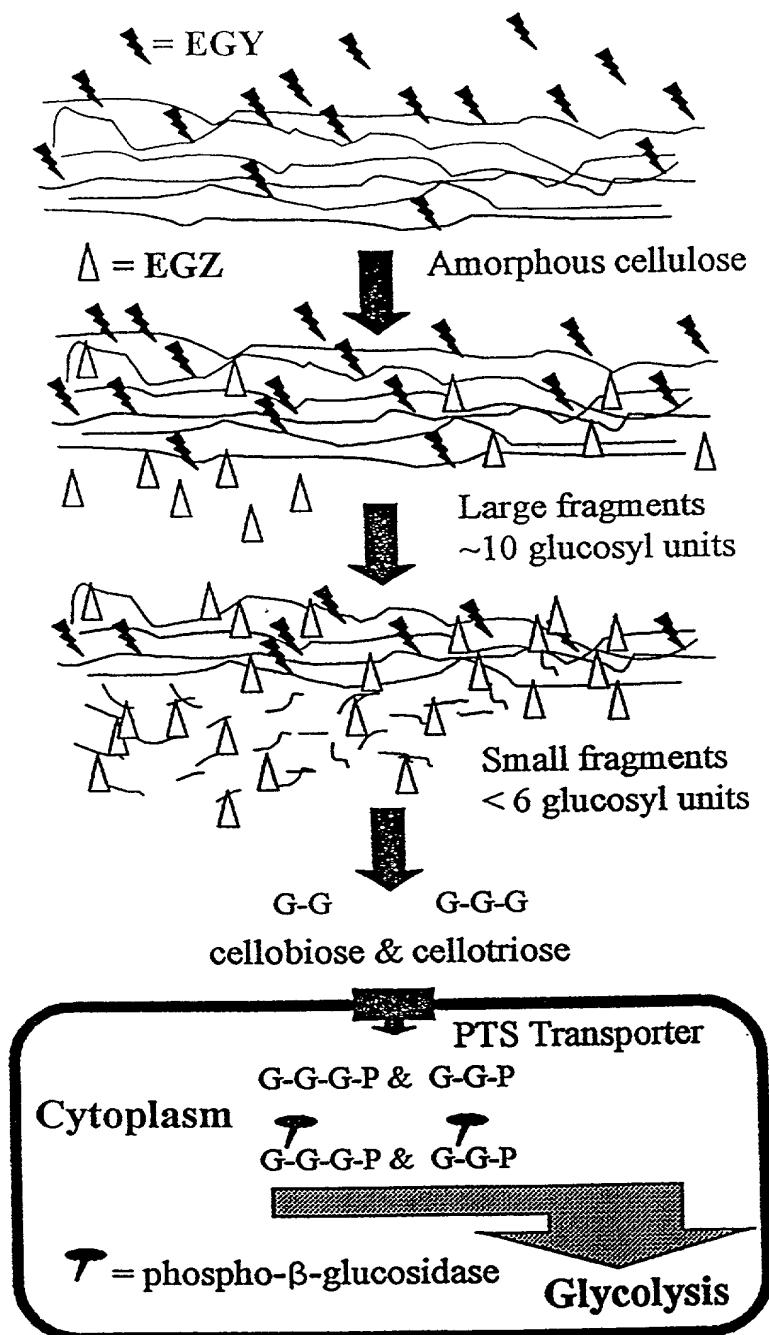


Fig. 13

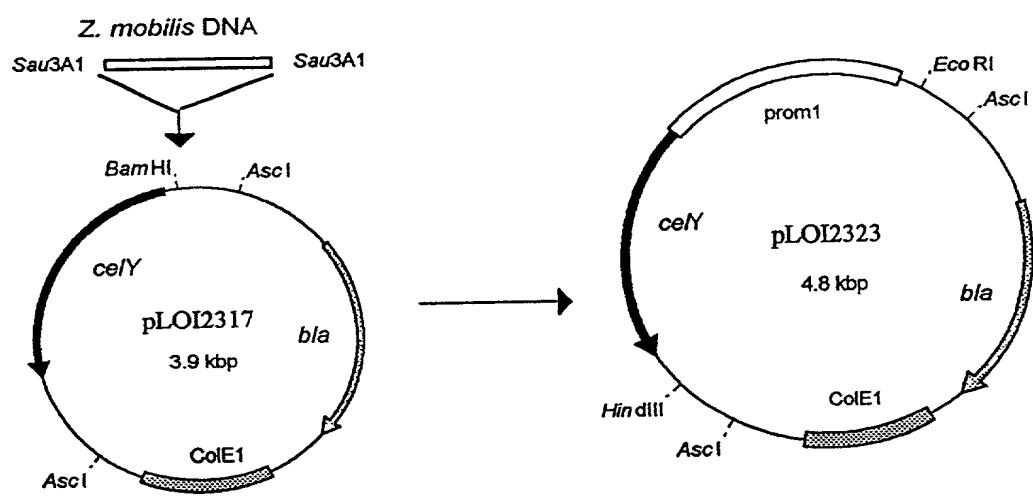


Fig. 14

Position (bp)	-35	-10	RNA	Proposed	δ factor consensus
			Start	δ factors	sequence
					-35 -10
ATATTITGATTTCAGAAAGCCTGATA <u>TCTTCCAACATCTT</u>		T (2)	δ^{70}	TTGACA	TATAAT
<u>GATTGATCCTCTAGAGTC</u> AACCTGCTTGTACTCGTGA <u>TCCAT</u>		A (4)	δ^{70}	TTGACA	TATAAT
<u>GAGTC</u> AAACCTGCTTGTACTCGTGA <u>TCCATT</u> ACAAGGGCGAA		C (1)	δ^{32}	CTTGAAA	CCCCAT
<u>TTACTCGTGTACACATT</u> ACAAGGGCGAA <u>TTAAATCGCCCTT</u>		C (3)	δ^{38}	CCGCCT	TATACT

Transcriptional starts for *ceiY* were identified by primer extension analysis. Four promoters were identified. Upstream sequence of these promoters with similarity to *E. coli* -35 and -10 regions are marked with underlines. RNA start sites are bolded. Putative promoters are numbered in parenthesis adjacent to the start site in descending order from the strongest. Differences in intensities were small, within 2-fold.

Fig. 15

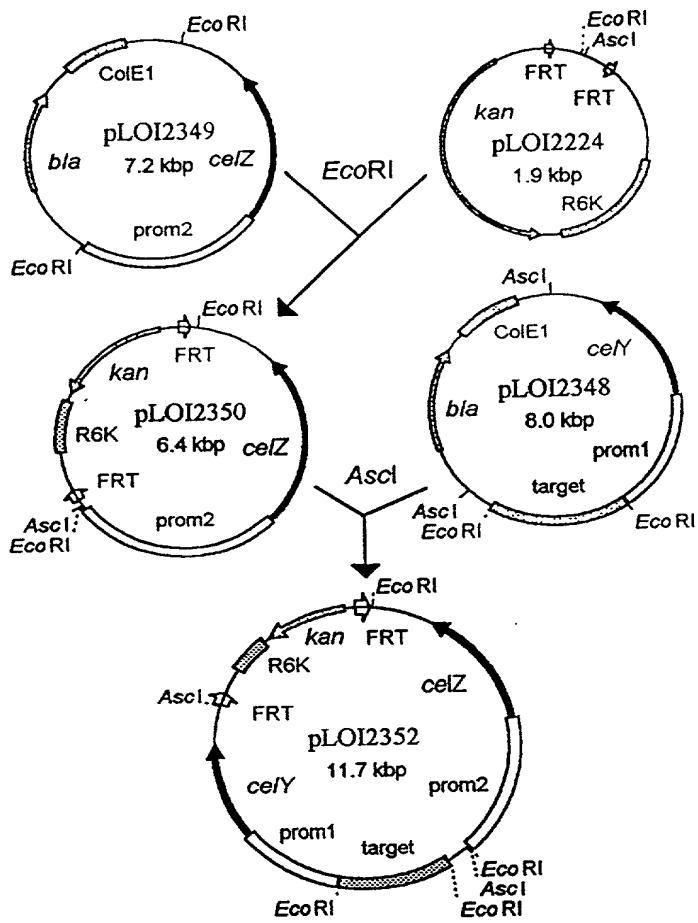


Fig. 16

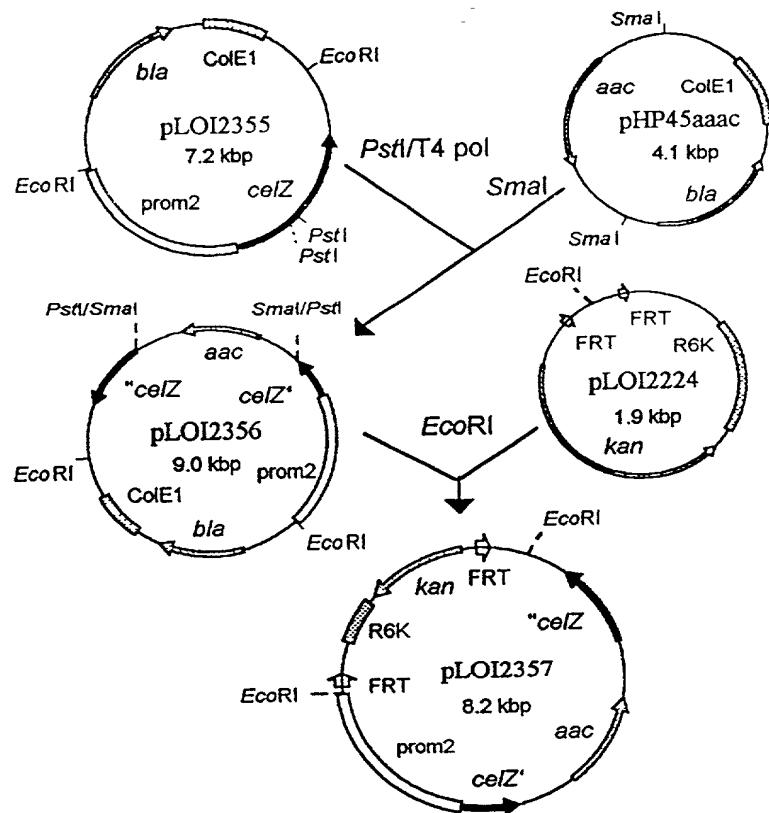


Fig. 17

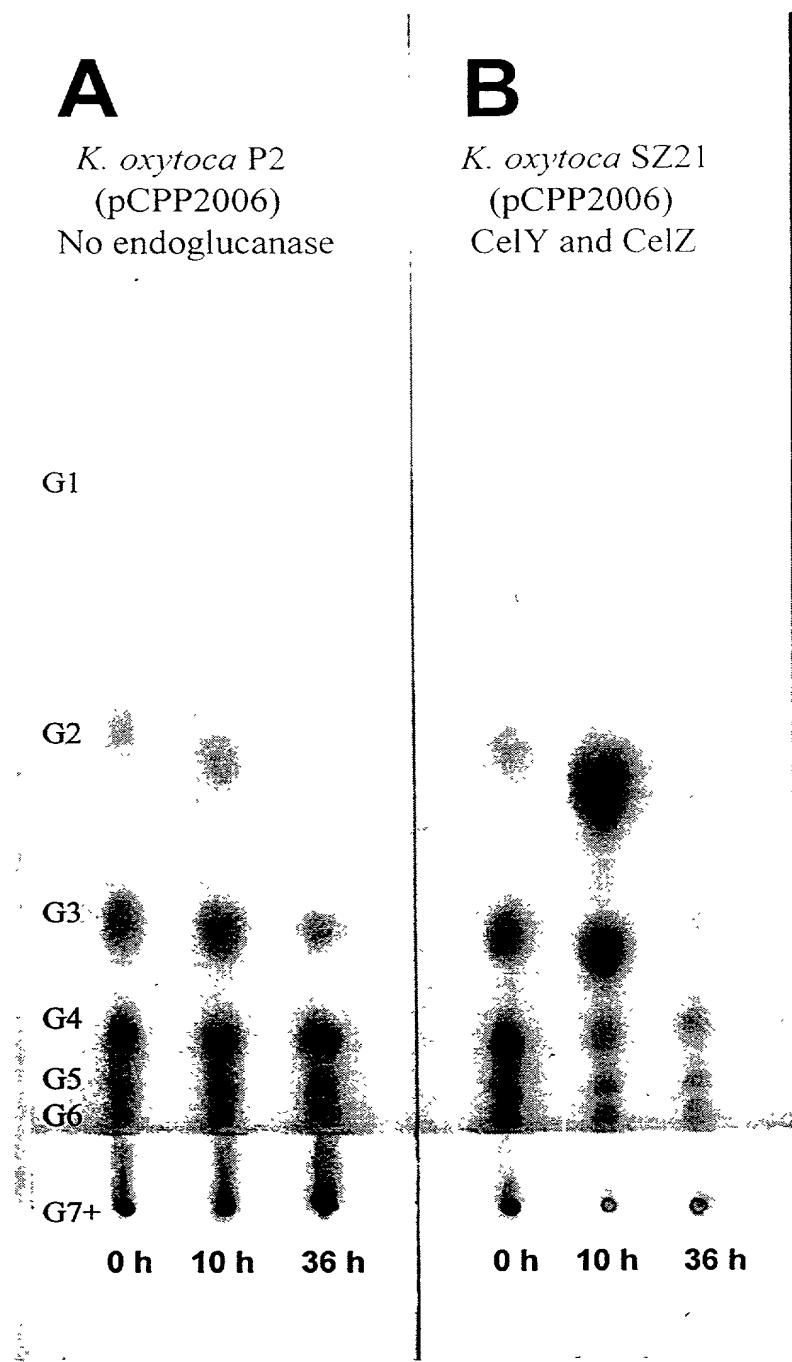


Fig. 18

